Lecture Notes in Bioinformatics 11183

Subseries of Lecture Notes in Computer Science

LNBI Series Editors

Sorin Istrail
Brown University, Providence, RI, USA

Pavel Pevzner
University of California, San Diego, CA, USA

Michael Waterman
University of Southern California, Los Angeles, CA, USA

LNBI Editorial Board

Søren Brunak
Technical University of Denmark, Kongens Lyngby, Denmark

Mikhail S. Gelfand
IITP, Research and Training Center on Bioinformatics, Moscow, Russia

Thomas Lengauer
Max Planck Institute for Informatics, Saarbrücken, Germany

Satoru Miyano
University of Tokyo, Tokyo, Japan

Eugene Myers
Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Marie-France Sagot
Université Lyon 1, Villeurbanne, France

David Sankoff
University of Ottawa, Ottawa, Canada

Ron Shamir
Tel Aviv University, Ramat Aviv, Tel Aviv, Israel

Terry Speed
Walter and Eliza Hall Institute of Medical Research, Melbourne, VIC, Australia

Martin Vingron
Max Planck Institute for Molecular Genetics, Berlin, Germany

W. Eric Wong
University of Texas at Dallas, Richardson, TX, USA

More information about this series at http://www.springer.com/series/5381

Mathieu Blanchette · Aïda Ouangraoua (Eds.)

Comparative Genomics

16th International Conference, RECOMB-CG 2018
Magog-Orford, QC, Canada, October 9–12, 2018
Proceedings

Springer

Editors
Mathieu Blanchette
McGill University
Montréal, QC
Canada

Aïda Ouangraoua
Université de Sherbrooke
Sherbrooke, QC
Canada

ISSN 0302-9743 ISSN 1611-3349 (electronic)
Lecture Notes in Bioinformatics
ISBN 978-3-030-00833-8 ISBN 978-3-030-00834-5 (eBook)
https://doi.org/10.1007/978-3-030-00834-5

Library of Congress Control Number: 2018954769

LNCS Sublibrary: SL8 – Bioinformatics

© Springer Nature Switzerland AG 2018
This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.
The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.
The publisher, the authors and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, express or implied, with respect to the material contained herein or for any errors or omissions that may have been made. The publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

This Springer imprint is published by the registered company Springer Nature Switzerland AG
The registered company address is: Gewerbestrasse 11, 6330 Cham, Switzerland

Preface

This volume contains the papers presented at RECOMBCG-18: the 16th RECOMB Comparative Genomics Satellite Workshop, held during October 9–12, 2018, in Magog-Orford, Québec, Canada.

There were 30 submissions. Each submission was reviewed by at least 4 reviewers, and some received up to 6 papers to review. The reviews were conducted by members of the Program Committee (PC) as well as by additional reviewers who were sought based on their expertise for specific papers. The PC decided to accept 18 papers. The program also included 6 invited talks and 2 poster sessions.

We thank the members of the Program Committee as well as the additional reviewers for their diligent work reviewing the manuscripts and conducting thorough discussions on the manuscripts and their reviews that informed the decision process.

We also thank the members of the Steering Committee, Marlia Braga, Dannie Durand, Jens Lagergren, Aoife McLysaght, Luay Nakhleh, and David Sankoff, for their guidance.

Special thanks go to the members of the Local Organizing Committee at the Université de Sherbrooke, Sarah Belhamiti, Alan Cohen, Ali Fotouhi, Jean-Michel Garant, Pierre-Étienne Jacques, Safa Jammali, Esaie Kuitche, Manuel Lafond, Lynn Lebrun, Jean-Pierre Perreault, Sébastien Rodrigue, Michelle Scott, Fanny Thuriot, Yves Tremblay, Anais Vannutelli, and Shengrui Wang, the students in particular, for all their efforts and generosity in organizing the conference.

Last but not least, we would like to thank the six keynote speakers who agreed to speak at the conference despite their very busy schedules: Belinda Chang, Dannie Durand, Daniel Durocher, Christian Landry, Gwenaël Piganeau, and Xavier Roucou.

The workshop would not have been possible without the generous contribution of our sponsors, whose support is greatly appreciated:

- Faculté de médecine et des sciences de la santé - Université de Sherbrooke
- Faculté des sciences - Université de Sherbrooke
- Programme de soutien à la tenue de colloques scientifiques étudiants - Université de Sherbrooke
- Fonds institutionnel de soutien aux activités étudiantes - Université de Sherbrooke
- Département d'informatique - Université de Sherbrooke
- Département de biochimie - Université de Sherbrooke
- Département de biologie - Université de Sherbrooke
- Calcul Québec

We used the EasyChair system for submissions, reviews, and proceedings formatting.

August 2018

Mathieu Blanchette
Aïda Ouangraoua

Organization

Program Chairs

Mathieu Blanchette	McGill University, Canada
Aida Ouangraoua	University of Sherbrooke, Canada

Steering Committee

Marília Braga	Bielefeld University, Germany
Dannie Durand	Carnegie Mellon University, USA
Jens Lagergren	Stockholm University, Sweden
Aoife McLysaght	Trinity College Dublin, Ireland
Luay Nakhleh	Rice University, USA
David Sankoff	University of Ottawa, Canada

Program Committee Members

Max Alekseyev	George Washington University, USA
Lars Arvestad	Stockholm University, Sweden
Sèverine Bérard	Université de Montpellier, France
Anne Bergeron	Université du Québec à Montréal, Canada
Marilia Braga	Bielefeld University, Germany
Alessandra Carbone	Sorbonne University, France
Cedric Chauve	Simon Fraser University, Canada
Leonid Chindelevitch	Simon Fraser University, Canada
Miklos Csuros	University of Montreal, Canada
Daniel Doerr	Bielefeld University, Germany
Dannie Durand	Carnegie Mellon University, USA
Ingo Ebersberger	Goethe University, Germany
Nadia El-Mabrouk	University of Montreal, Canada
Oliver Eulenstein	Iowa State University, USA
Guillaume Fertin	CNRS, University of Nantes, France
Pawel Gorecki	University of Warsaw, Poland
Michael Hallett	Concordia University, Canada
Katharina Jahn	ETH Zurich, Switzerland
Asif Javed	Genome Institute of Singapore (A-STAR), Singapore
Manuel Lafond	University of Sherbrooke, Canada
Jens Lagergren	KTH Royal Institute of Technology, Sweden
Kevin Liu	Michigan State University, USA
Fábio H. V. Martinez	Universidade Federal de Mato Grosso do Sul, Brazil
Joao Meidanis	University of Campinas and Scylla Bioinformatics, Brazil
István Miklós	Rényi Institute, Hungary

Luay Nakhleh	Rice University, USA
David Sankoff	University of Ottawa, Canada
Eric Tannier	Inria, France
Glenn Tesler	University of California San Diego, USA
Olivier Tremblay-Savard	University of Manitoba, Canada
Jens Stoye	Bielefeld University, Germany
Krister Swenson	CNRS and Université de Montpellier, France
Tamir Tuller	Tel Aviv University, Israel
Jean-Stéphane Varré	University of Lille, France
Lusheng Wang	City University of Hong Kong, SAR China
Tandy Warnow	University of Illinois at Urbana-Champaign, USA
Louxin Zhang	National University of Singapore, Singapore
Jie Zheng	ShanghaiTech University, China

Also a big thank you to our sub-reviewers: Sergey Aganezov, Eloi Araujo, Maria Atamanova, Pavel Avdeyev, Annie Chateau, Sarah Christensen, Riccardo Dondi, Philippe Gambette, Hussein Hejase, Géraldine Jean, Yu Lin, Bernard Moret, Agnieszka Mykowiecka, Anton Nekhai, Fabio Pardi, Jarek Paszek, Diego P. Rubert, Celine Scornavacca, Marco Stefanes, Riccardo Vicedomini, Roland Wittler, and João Paulo Pereira Zanetti.

Local Organizing Committee

Mathieu Blanchette	McGill University, Canada
Aïda Ouangraoua	University of Sherbrooke, Canada
Sarah Belhamiti	University of Sherbrooke, Canada
Alan Cohen	University of Sherbrooke, Canada
Ali Fotouhi	University of Sherbrooke, Canada
Jean-Michel Garant	University of Sherbrooke, Canada
Pierre-Étienne Jacques	University of Sherbrooke, Canada
Safa Jammali	University of Sherbrooke, Canada
Esaie Kuitche	University of Sherbrooke, Canada
Manuel Lafond	University of Ottawa and University of Sherbrooke, Canada
Jean-Pierre Perreault	University of Sherbrooke, Canada
Sébastien Rodrigue	University of Sherbrooke, Canada
Michelle Scott	University of Sherbrooke, Canada
Fanny Thuriot	University of Sherbrooke, Canada
Anais Vannutelli	University of Sherbrooke, Canada
Shengrui Wang	University of Sherbrooke, Canada

Contents

Genome Rearrangements

A Cubic Algorithm for the Generalized Rank Median of Three Genomes. . . . 3
Leonid Chindelevitch and Joao Meidanis

The Rooted SCJ Median with Single Gene Duplications 28
Aniket C. Mane, Manuel Lafond, Pedro Feijão, and Cedric Chauve

A General Framework for Genome Rearrangement
with Biological Constraints. 49
Pijus Simonaitis, Annie Chateau, and Krister M. Swenson

Estimation of the True Evolutionary Distance Under the INFER Model 72
Alexey Zabelkin and Nikita Alexeev

Genome Sequencing

On the Hardness of Approximating Linearization of Scaffolds Sharing
Repeated Contigs 91
Tom Davot, Annie Chateau, Rodolphe Giroudeau, and Mathias Weller

Detecting Large Indels Using Optical Map Data 108
Xian Fan, Jie Xu, and Luay Nakhleh

Applied Comparative Genomics

mClass: Cancer Type Classification with Somatic Point Mutation Data 131
Md Abid Hasan and Stefano Lonardi

Speciation and Rate Variation in a Birth-and-Death Account of WGD
and Fractionation; the Case of Solanaceae 146
Yue Zhang, Chunfang Zheng, and David Sankoff

Reconciliation and Coalescence

Detecting Introgression in Anopheles Mosquito Genomes
Using a Reconciliation-Based Approach. 163
Cedric Chauve, Jingxue Feng, and Liangliang Wang

Reconstructing the History of Syntenies Through Super-Reconciliation 179
Mattéo Delabre, Nadia El-Mabrouk, Katharina T. Huber, Manuel Lafond, Vincent Moulton, Emmanuel Noutahi, and Miguel Sautie Castellanos

On the Variance of Internode Distance Under the Multispecies Coalescent . . . 196
Sébastien Roch

Phylogenetics

Linear-Time Algorithms for Some Phylogenetic Tree Completion Problems Under Robinson-Foulds Distance 209
Mukul S. Bansal

Multi-SpaM: A Maximum-Likelihood Approach to Phylogeny Reconstruction Using Multiple Spaced-Word Matches and Quartet Trees 227
Thomas Dencker, Chris-André Leimeister, Michael Gerth, Christoph Bleidorn, Sagi Snir, and Burkhard Morgenstern

FastNet: Fast and Accurate Statistical Inference of Phylogenetic Networks Using Large-Scale Genomic Sequence Data 242
Hussein A. Hejase, Natalie VandePol, Gregory M. Bonito, and Kevin J. Liu

NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees 260
Erin K. Molloy and Tandy Warnow

On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem 277
Dikshant Pradhan and Mohammed El-Kebir

Non-parametric and Semi-parametric Support Estimation Using SEquential RESampling Random Walks on Biomolecular Sequences 294
Wei Wang, Jack Smith, Hussein A. Hejase, and Kevin J. Liu

Linear-Time Tree Containment in Phylogenetic Networks 309
Mathias Weller

Author Index 325